

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAARmaqzj: 2054 aa  
>LEX 289\_SEQ ID NO:2  
vs /tmp/fastaDAASmaqzj library  
searching /tmp/fastaDAASmaqzj library

1958 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 42, opt: 30, gap-pen: -12/ -2, width: 16

Scan time: 0.066

The best scores are:

opt

LEX 289\_SEQ ID NO:4

(1958) 12639

>>LEX 289\_SEQ ID NO:4

(1958 aa)

initn: 12639 init1: 12639 opt: 12639

Smith-Waterman score: 12639; 100.000% identity in 1945 aa overlap (1-1945:1-1945)

	10	20	30	40	50	60
LEX	MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE					
	10	20	30	40	50	60
LEX	MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE					
	70	80	90	100	110	120
LEX	ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG					
	70	80	90	100	110	120
LEX	ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG					
	130	140	150	160	170	180
LEX	DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG					
	130	140	150	160	170	180
LEX	DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG					
	190	200	210	220	230	240
LEX	DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF					
	190	200	210	220	230	240
LEX	DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF					
	250	260	270	280	290	300
LEX	GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWWSVGVIAYEMIYGR					
	250	260	270	280	290	300
LEX	GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWWSVGVIAYEMIYGR					
	310	320	330	340	350	360
LEX	SPFAEGTSARTFNNIMNFQRFKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF					
	310	320	330	340	350	360
LEX	SPFAEGTSARTFNNIMNFQRFKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF					

	370	380	390	400	410	420
LEX	SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGF					
LEX	SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
LEX	YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVS					
LEX	YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVS					
	430	440	450	460	470	480
	490	500	510	520	530	540
LEX	EVEAVLSQKEVELKASETQRSLLLEQDLATYITECSSLKRSLEQARMEVSQEDDKALQLLH					
LEX	EVEAVLSQKEVELKASETQRSLLLEQDLATYITECSSLKRSLEQARMEVSQEDDKALQLLH					
	490	500	510	520	530	540
	550	560	570	580	590	600
LEX	DIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEFK					
LEX	DIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEFK					
	550	560	570	580	590	600
	610	620	630	640	650	660
LEX	RKATECQHKLKAKDQKGPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTEATELLQ					
LEX	RKATECQHKLKAKDQKGPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTEATELLQ					
	610	620	630	640	650	660
	670	680	690	700	710	720
LEX	NIRQAKERAERELEKLQNREDSSEGIRKKLVEAEERRHSLENKVKRLETMERRENRLKDD					
LEX	NIRQAKERAERELEKLQNREDSSEGIRKKLVEAEERRHSLENKVKRLETMERRENRLKDD					
	670	680	690	700	710	720
	730	740	750	760	770	780
LEX	IQTQSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEEKIKVLDNQIKKDLAD					
LEX	IQTQSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEEKIKVLDNQIKKDLAD					
	730	740	750	760	770	780
	790	800	810	820	830	840
LEX	KETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT					
LEX	KETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT					
	790	800	810	820	830	840
	850	860	870	880	890	900
LEX	QRNMKAQEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSKDNRLLELETRL					
LEX	QRNMKAQEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSKDNRLLELETRL					
	850	860	870	880	890	900
	910	920	930	940	950	960
LEX	REVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQAKTELEETAE					
LEX	REVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQAKTELEETAE					
	910	920	930	940	950	960

	970	980	990	1000	1010	1020
LEX	EEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEAS					
LEX	EEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEAS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
LEX	GANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLE					
LEX	GANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLE					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
LEX	KERQWEAWRSVLGDEKSQFECRVRELQRMLEDTEKQSRARADQRITESRQVVELAVKEHKA					
LEX	KERQWEAWRSVLGDEKSQFECRVRELQRMLEDTEKQSRARADQRITESRQVVELAVKEHKA					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
LEX	EILALQQALKEQKLAESLSDKLNDLEKKHAMLEMNARSLQQKLETERELKQRLLEEQA					
LEX	EILALQQALKEQKLAESLSDKLNDLEKKHAMLEMNARSLQQKLETERELKQRLLEEQA					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
LEX	LQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTISQ					
LEX	LQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTISQ					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
LEX	QTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEKEKARCAELEEALQKTRIELRSAREEA					
LEX	QTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEKEKARCAELEEALQKTRIELRSAREEA					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350	1360	1370	1380
LEX	AHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSLAPPSSRRKESSTPEEFSRRL					
LEX	AHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSLAPPSSRRKESSTPEEFSRRL					
	1330	1340	1350	1360	1370	1380
	1390	1400	1410	1420	1430	1440
LEX	KERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCGL					
LEX	KERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCGL					
	1390	1400	1410	1420	1430	1440
	1450	1460	1470	1480	1490	1500
LEX	PAEYATHFTEAFCDKMNPSGLQTKEPSSSLHLEGWMKVPRNNKRGQQGWDKRYIVLEGS					
LEX	PAEYATHFTEAFCDKMNPSGLQTKEPSSSLHLEGWMKVPRNNKRGQQGWDKRYIVLEGS					
	1450	1460	1470	1480	1490	1500
	1510	1520	1530	1540	1550	1560
LEX	KVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYILKMESHPT					
LEX	KVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYILKMESHPT					
	1510	1520	1530	1540	1550	1560

```

      1570      1580      1590      1600      1610      1620
LEX    TCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDRDL
      .....
LEX    TCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDRDL
      1570      1580      1590      1600      1610      1620

      1630      1640      1650      1660      1670      1680
LEX    MNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA
      .....
LEX    MNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA
      1630      1640      1650      1660      1670      1680

      1690      1700      1710      1720      1730      1740
LEX    LCLVDVKVKVQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLCICAAMPSKVVIL
      .....
LEX    LCLVDVKVKVQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLCICAAMPSKVVIL
      1690      1700      1710      1720      1730      1740

      1750      1760      1770      1780      1790      1800
LEX    RYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLEEFLDKNDHSLA
      .....
LEX    RYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLEEFLDKNDHSLA
      1750      1760      1770      1780      1790      1800

      1810      1820      1830      1840      1850      1860
LEX    PAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAFA
      .....
LEX    PAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAFA
      1810      1820      1830      1840      1850      1860

      1870      1880      1890      1900      1910      1920
LEX    YREPYL FVTHFNSLEVEIQARSSAGTPARAYLDIPNPRYLGPASSGAIYLASSYQDKL
      .....
LEX    YREPYL FVTHFNSLEVEIQARSSAGTPARAYLDIPNPRYLGPASSGAIYLASSYQDKL
      1870      1880      1890      1900      1910      1920

      1930      1940      1950      1960      1970      1980
LEX    RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPTYNEHITKRVASSPAPPEGPSHPREP
      .....
LEX    RVICCKGNLVKESGTEHHRGPSTSRRFQSHMARDEYKP
      1930      1940      1950

```

2054 residues in 1 query sequences

1958 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon Oct 6 14:52:57 2003 done: Mon Oct 6 14:53:00 2003

Scan time: 0.066 Display time: 5.550

Function used was FASTA